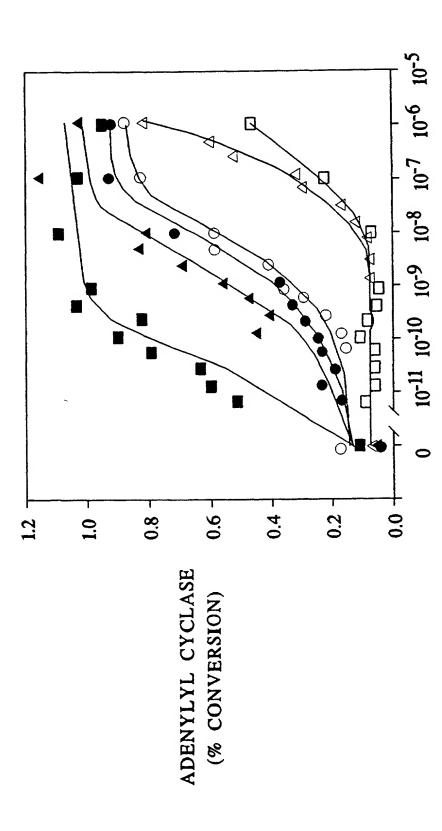
Fig. 1A

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AGTGAGAACA AGAAAGCAAA GAGCAGACTC TTTCAACTGA GAATGAATAT TTTGAAGCCC	180
AAGATTTTAA AGTGATGATG ATTAGAGTCG TACCTAAAAG AGACTAAAAA CTCCATGTCA	240
AGCTCTGGAC TTGTGACATT TACTCACAGC AGGCATGGCA ATTTTAGCCT CACAACTTTC	300
AGACAGATAA AGACTTGGAG GAAATAACTG AGACGACTCC CTGACCCAGG AGGTTAAATC	360
AATTCAGGGG GACACTGGAA TTCTCCTGCC AGC ATG GTG AAC TCC ACC CAC CGT Met Val Asn Ser Thr His Arg 1 5	414
GGG ATG CAC ACT TCT CTG CAC CTC TGG AAC CGC AGC AGT TAC AGA CTG Gly Met His Thr Ser Leu His Leu Trp Asn Arg Ser Ser Tyr Arg Leu 10 15 20	462
CAC AGC AAT GCC AGT GAG TCC CTT GGA AAA GGC TAC TCT GAT GGA GGG His Ser Asn Ala Ser Glu Ser Leu Gly Lys Gly Tyr Ser Asp Gly Gly 25 ' 30	510
TGC TAC GAG CAA CTT TTT GTC TCT CCT GAG GTG TTT GTG ACT CTG GGT Cys Tyr Glu Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly 45 50 55	558
GTG ATC AGC TTG TTG GAG AAT ATC TTA GTG ATT GTG GCA ATA GCC AAG Val Ile Ser Leu Leu Glu Asn Ile Leu Val Ile Val Ala Ile Ala Lys 60 65 70	606
AAC AAG AAT CTG CAT TCA CCC ATG TAC TTT TTC ATC TGC AGC TTG GCT Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala 75	654
GTG GCT GAT ATG CTG GTG AGC GTT TCA AAT GGA TCA GAA ACC ATT ATC Val Ala Asp Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile 90 95 100	702
ATC ACC CTA TTA AAC AGT ACA GAT ACG GAT GCA CAG AGT TTC ACA GTG 11e Thr Leu Leu Asn Ser Thr Asp Thr Asp Ala Gln Ser Phe Thr Val 105 110 115	750
AAT ATT GAT AAT GTC ATT GAC TCG GTG ATC TGT AGC TCC TTG CTT GCA Asn Ile Asp Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala 120 135	798
TCC ATT TGC AGC CTG CTT TCA ATT GCA GTG GAC AGG TAC TTT ACT ATC Ser Ile Cys Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile 140 145 150	846
TTC TAT GCT CTC CAG TAC CAT AAC ATT ATG ACA GTT AAG CGG GTT GGG Phe Tyr Ala Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly 155 160 165	894
ATC AGC ATA AGT TGT ATC TGG GCA GCT TGC ACG GTT TCA GGC ATT TTG Ile Ser Ile Ser Cys Ile Trp Ala Ala Cys Thr Val Ser Gly Ile Leu	942

Fig. 1B

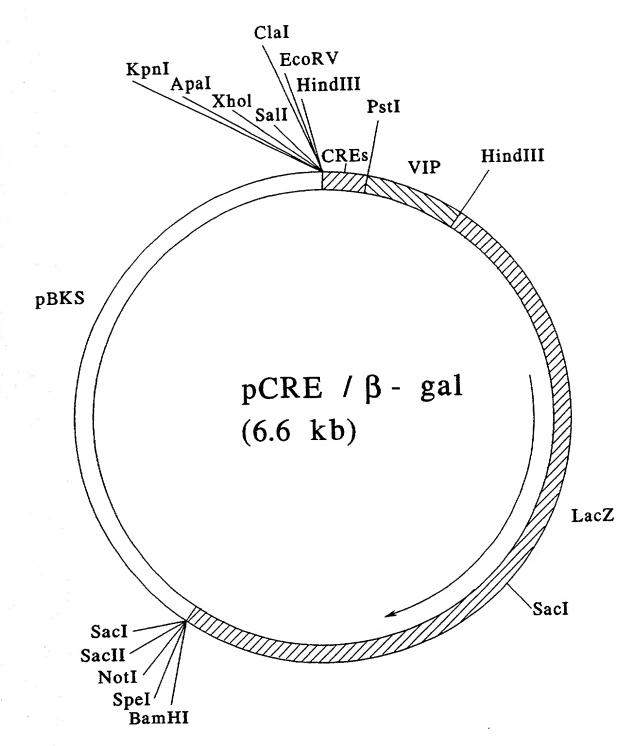
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	TTC Phe															1	1038
	CTG Leu															;	1086
ACT Thr	GGT Gly	GCC Ala	ATC Ile 235	CGC Arg	CAA Gln	GGT Gly	GCC Ala	AAT Asn 240	ATG Met	AAG Lys	GGA Gly	GCG Ala	ATT Ile 245	ACC Thr	TTG Leu	1	1134
	ATC Ile															:	1182
CAC His	TTA Leu 265	ATA Ile	TTC Phe	TAC Tyr	ATC Ile	TCT Ser 270	TGT Cys	CCT Pro	CAG Gln	AAT Asn	CCA Pro 275	TAT Tyr	TGT Cys	GTG Val	TGC Cys	:	1230
	ATG Met															,	1278
ATC Ile	ATC Ile	GAT Asp	CCT Pro	CTG Leu 300	ATT Ile	TAT Tyr	GCA Ala	CTC Leu	CGG Arg 305	AGT Ser	CAA Gln	GAA Glu	CTG Leu	AGG Arg 310	AAA Lys	:	1326
ACC Thr	TTC Phe	AAA Lys	GAG Glu 315	ATC Ile	ATC Ile	TCT Ser	TCC Ser	TAT Tyr 320	CCC Pro	CTG Leu	GGA Gly	GGC Gly	CTT Leu 325	TGT Cys	GAC Asp	3	1374
	TCT Ser				TAAJ	\TGG(GA (CAGAC	CAC	gc aj	\TAT/	(GGA)	A CAS	rcca:	raag	:	1429
AGA	CTTT	PTC A	ACTC:	TTAC	CC TA	CCT	SAAT/	A TTO	TACT	rrcr	GCA	CAG	TT :	rcrc.	rrccg1	r :	1489
GTA	GGGT	ACT (GTT(GAGA:	TA TO	CAT	rgrg	KAA 1	ATTI	AAGC	CTAT	'GAT'	rr :	TAAT	GAGAA	A :	1549
AAA	TGCC	CAG 1	rcrc.	IGTA:	TT A	rtrc	CAATO	TC	ATGCT	TACT	TTT	rtgg	CA 1	raaai	ATATG	A :	1609
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TT																:	1671

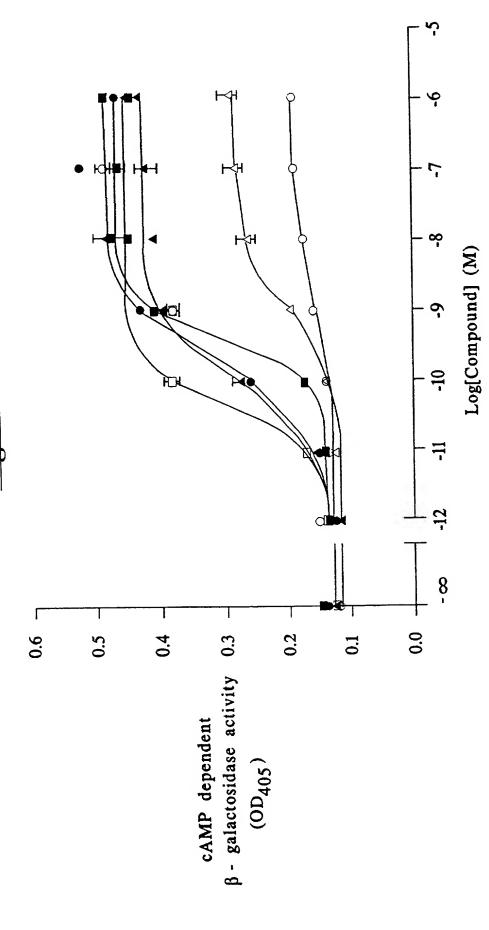




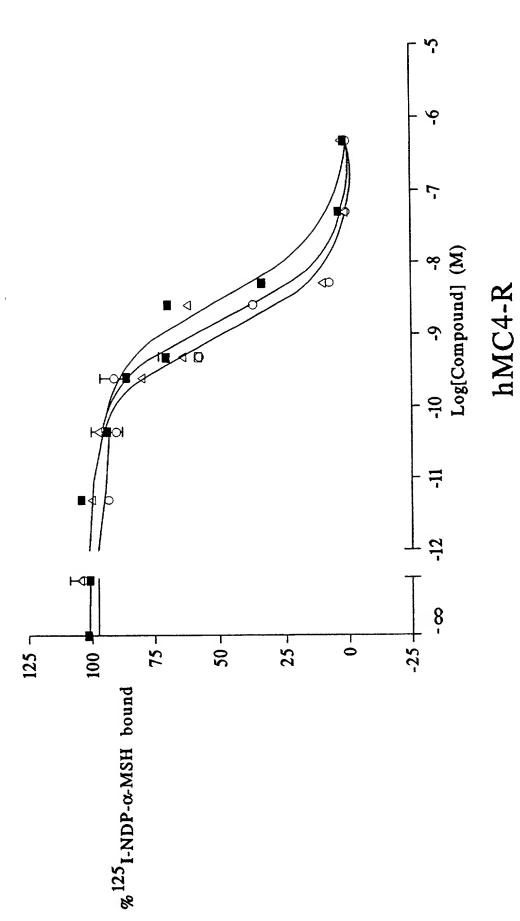
[PEPTIDE] (M)

Fig. 3





hMC4-R





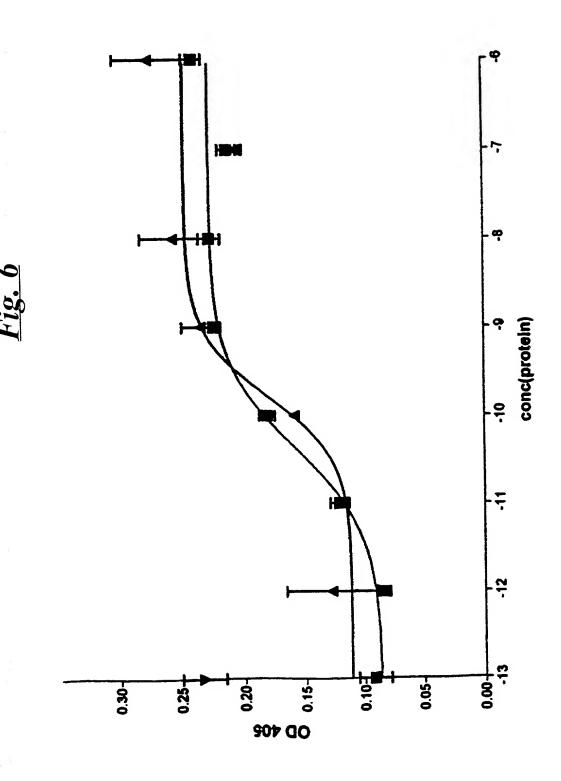
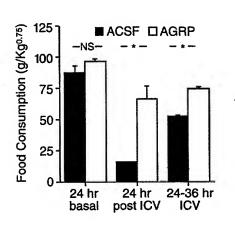
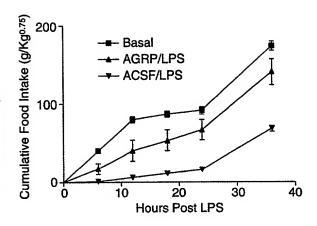
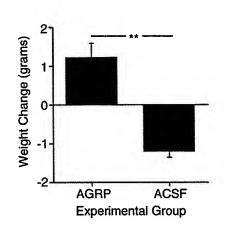


Fig. 7A

Fig. 7*B*







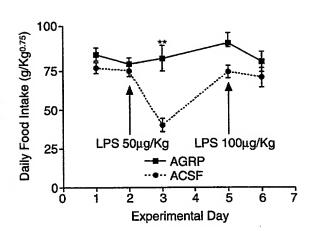


Fig. 7C

Fig. 7D

Fig. 8A

Fig. 8B

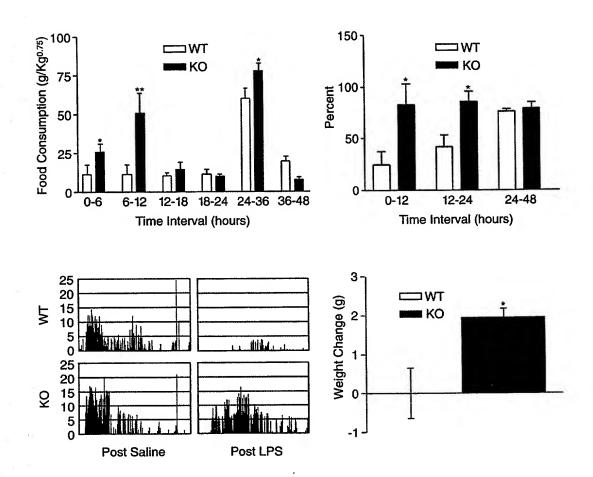


Fig. 8C

Fig. 8D

Adrenal Stress Response to LPS in MC4-RKO Mice

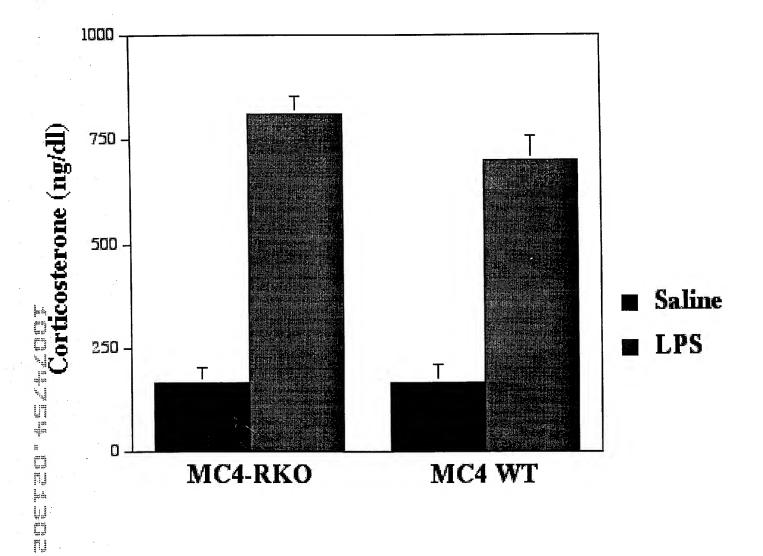
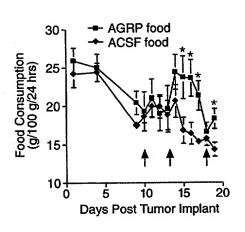
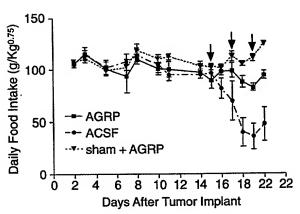


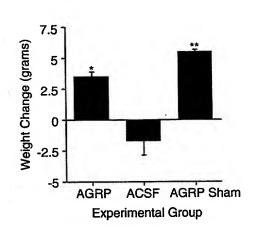
Fig. 8*E*

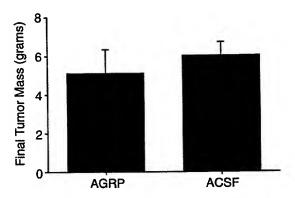
Fig. 9A

Fig. 9B









<u>Fig. 9C</u>

Fig. 9D

Fig. 10A

Fig. 10B

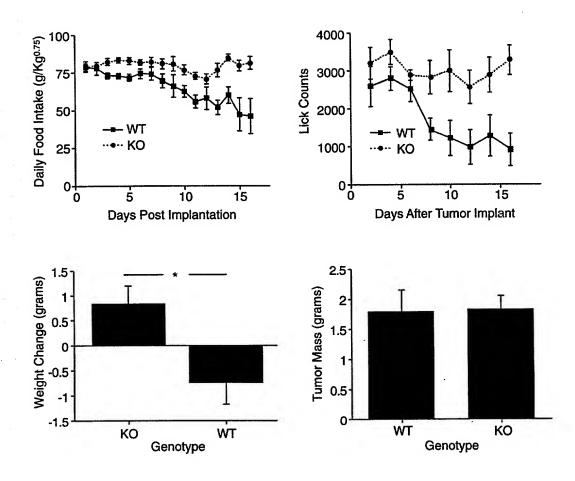


Fig. 10C

Fig. 10D

Carcass Weight Change During Tumor Growth

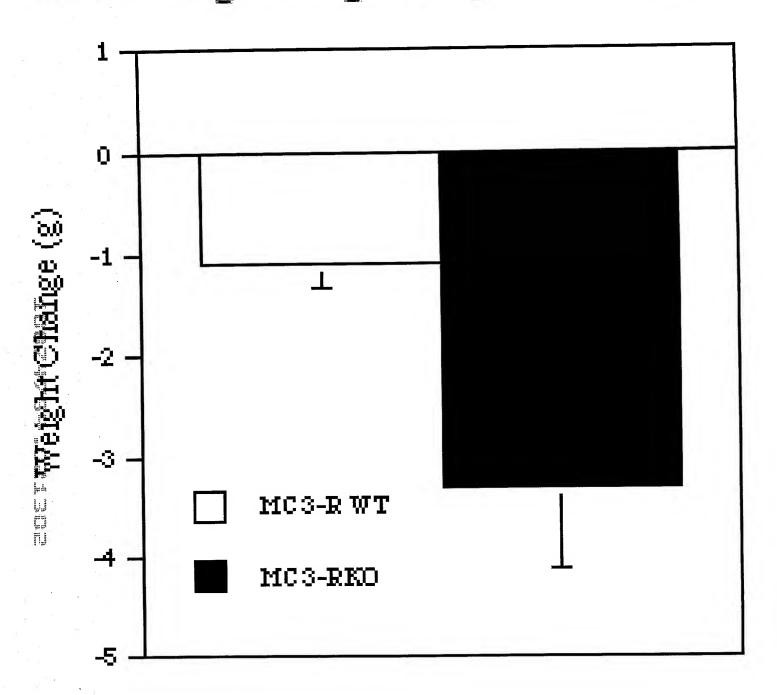


Fig. 10E

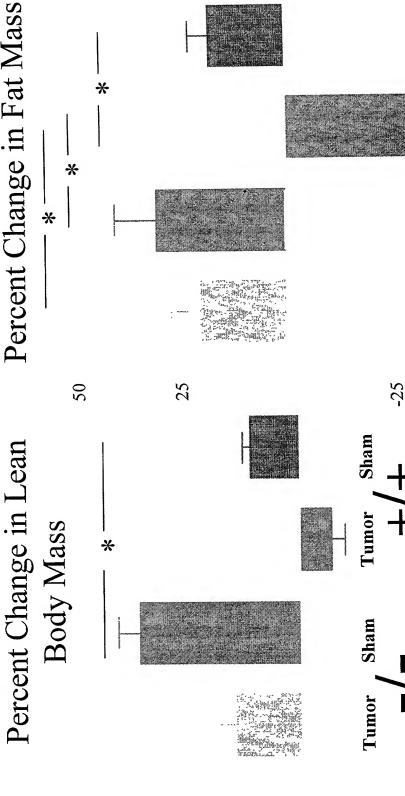
DEXA Body Composition

Fig. 114

20

Analysis Fig. 11B

Percent Change in Fat Mass



10

ANOVA p<0.005. *p<0.01 post hoc

Tumor

Sham

Metabolic Response to LPS in MC4-RKO Mice

